

Marked-Up Copy of Amended Specification:

New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package [(available at <http://www.gcg.com>)], using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (Devereux, J., *et al.*, *Nucleic Acids Res.* 12(1):387 (1984)) [(available at <http://www.gcg.com>)], using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against sequence databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (*J. Mol. Biol.* 215:403-10 (1990)). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, word length = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, word length = 3 to obtain amino acid sequences homologous to the proteins of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (*Nucleic Acids Res.* 25(17):3389-3402 (1997)). When utilizing BLAST

and gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. [See <http://www.ncbi.nlm.nih.gov>.]

REMARKS**Objections to the Specification**

The examiner stated that the disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant has hereby deleted the embedded hyperlink and/or other form of browser-executable code. A clean copy and a marked-up copy are submitted above.

Double Patenting Rejection

The Examiner rejected claims 4, 6, 8, 22-26 under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-20 of copending Application No. 09/618,893. The Examiner stated that although the conflicting claims are not identical, they are not patentably distinct from each other because the claims of copending application comprise SEQ ID Nos: 85-87 which match absolutely with the SEQ ID Nos. 853-855 of the instant claims.

Applicants will delete the SEQ ID Nos: 85-87 in the claims of Serial No: 09/618,893, pending that claims of the present application are allowed.

Rejections under 35 USC 102

The Examiner rejected claims 4, 6, 8 and 22-26 under 35 U.S.C. 102(f) because the claims drawn to isolated nucleic acid molecules consisting of SEQ ID Nos: 853-855 of instant invention match absolutely with the SEQ ID Nos: 85, 86 and 87 of copending application NO: 09/618,893 and with SEQ ID Nos: 16753 and 16574 of copending application NO. 09/614, 150.

Applicants respectfully disagree. These two applications cannot be prior art against the present application. The present application claims priority at least to one provisional application filed on March 3, 2000 (Application NO: 60/187, 241). The SEQ ID NOs: 853-855 of the present invention correspond to SEQ ID NO: 1314-1316 in the application NO: 60/187, 241. The sequences in application NO: 09/618,893 or in application NO: 09/614, 150 that have absolute match to the claimed sequence of the

instant invention were either disclosed later, if not the same time, than the priority date of the present application. Therefore, application NO: 09/618,893 and application NO. 09/614, 150 do not constitute prior art to the present application. The rejection should be withdrawn.

For the same reason, Applicants respectfully request the withdrawal of the rejection under 35 U.S.C 102(e). Because the sequences in the claims of the present application were filed on March 3, 2000, and the sequences in application NO: 09/614,150 that have absolute match to the claimed sequences of the instant invention were disclosed later, if not the same time, than the priority date of the present invention, application NO. 09/614, 150 (the Venter application) is no longer prior art to the present invention.

In addition, the Venter application was not yet published, and since 102(e) requires published patents or applications as prior art, therefore, the rejection under 102(e) is not applicable.

Applicants respectfully request the withdrawal of the rejection under 103(a) as obvious over Venter et al (application number 09/614,150). Since the 102(e) art is no longer applicable, the rejection under 103(a) should be withdrawn. Moreover, the examiner has acknowledged (on page 4, last paragraph) that the present application and application NO. 09/614, 150 has a common assignee, thus, under 35 USC103(c), the 103 (a) rejection should be withdrawn because 103 (c) state that subject matter developed by another person, which qualifies as prior art only under one or more of subsections (e), (f), and (g) of section 102 of this title, shall not preclude patentability under this section where the subject matter and the claimed invention were, at the time the invention was made, owned by the same person or subject to an obligation of assignment to the same person.


In view of the above, Applicants believe the present application is in the condition for allowance. Applicants respectfully request that the Examiner reconsider and withdraw the rejections of the claims, and issue a Notice of Allowance at the earliest convenience.

Serial No. 09/619,049

Respectfully submitted,
CELERA GENOMICS

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